

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/830,972 A
Source: JFW16
Date Processed by STIC: 01/05/2006

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,972A

DATE: 01/05/2006
TIME: 12:26:40

Input Set : E:\10200-003-999.txt
Output Set: N:\CRF4\01052006\I830972A.raw

4 <110> APPLICANT: Schwab, M.
 5 Chen, M.
 7 <120> TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO
 8 GENES AND METHODS BASED THEREON
 10 <130> FILE REFERENCE: 10200-003-999
 12 <140> CURRENT APPLICATION NUMBER: 09/830,972A
 13 <141> CURRENT FILING DATE: 2001-09-24
 15 <150> PRIOR APPLICATION NUMBER: PCT/US99/26160
 16 <151> PRIOR FILING DATE: 1999-11-05
 18 <150> PRIOR APPLICATION NUMBER: 60/107,446
 19 <151> PRIOR FILING DATE: 1998-11-06
 21 <160> NUMBER OF SEQ ID NOS: 51
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 3741
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Rattus sp.
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (253) . . . (3741)
 34 <400> SEQUENCE: 1
 35 attgctcgtc tgggcggcgg cggcggctgc agcctgggac agggcgggtg gcacatctcg 60
 36 atcgcgaagg cagcagaagc agtctcatgt ttccgggagc cgtcgcctct gcaggttctt 120
 37 cggctcggct cggcacgact cggcctgcct ggccctgcct agtcttgccc aacccccaca 180
 38 accggcccgcg actctgagga gaagcggccc tgcggcggct gtagctgcag catcgctggc 240
 39 gaccggccag cc atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc 291
 40 Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser
 41 1 5 10
 43 acg gac agc ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg 339
 44 Thr Asp Ser Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val
 45 15 20 25
 47 acg gag ccc gag gac gag gag gag gag gag gag gag gag 387
 48 Thr Glu Pro Glu Asp Glu Asp Glu Glu Glu Glu Asp Glu Glu
 49 30 35 40 45
 51 gag gac gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc 435
 52 Glu Asp Asp Glu Asp Leu Glu Leu Glu Val Leu Glu Arg Lys Pro
 53 50 55 60
 55 gca gcc ggg ctg tcc gca gct gcg gtg ccg ccc gcc gcc gca gca 483
 56 Ala Ala Gly Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro
 57 65 70 75
 58 ctg ctg gac ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg 531
 59 Leu Leu Asp Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro
 60 80 85 90

Cp9-6)

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62	ctg ccg gcc gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa	579
63	Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu	
64	95 100 105	
66	cgc agc ccc gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc	627
67	Arg Ser Pro Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val	
68	110 115 120 125	
70	ctg ccc tcc aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg	675
71	Leu Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro	
72	130 135 140	
74	cct ccg ccg cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc	723
75	Pro Pro Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro	
76	145 150 155	
78	cct tcc acg ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat	771
79	Pro Ser Thr Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp	
80	160 165 170	
82	gag acc ctt ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc	819
83	Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser	
84	175 180 185	
86	tct gca gaa aaa att atg gat ttg atg gag cag cca ggt aac act gtt	867
87	Ser Ala Glu Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val	
88	190 195 200 205	
90	tcg tct ggt caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc	915
91	Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala	
92	210 215 220	
94	tct ctt cct tct cta tct ctc tca act gtt tct ttt aaa gaa cat	963
95	Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His	
96	225 230 235	
98	gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca att	1011
99	Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile	
100	240 245 250	
102	gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg gca aca	1059
103	Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr	
104	255 260 265	
106	aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat	1107
107	Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr	
108	270 275 280 285	
110	tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc	1155
111	Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala	
112	290 295 300	
113	ata tta gta gaa aac act aag gaa gaa gta att gtg agg agt aaa gac	1203
114	Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp	
115	305 310 315	
117	aaa gag gat tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca	1251
118	Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser	
119	320 325 330	
121	cct gtg ggt aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac	1299
122	Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp	
123	335 340 345	
125	att ttt aat gaa atg cag atg tca gta gta gca cct gtg agg gaa gag	1347

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126	Ile Phe Asn Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu	
127	350 355 360 365	
129	tat gca gac ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act	1395
130	Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr	
131	370 375 380	
133	tat gag gga agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt	1443
134	Tyr Glu Gly Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser	
135	385 390 395	
137	aaa gtg gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt	1491
138	Lys Val Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu	
139	400 405 410	
141	ggg aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc	1539
142	Gly Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr	
143	415 420 425	
145	cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc	1587
146	Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser	
147	430 435 440 445	
149	ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct ttg tta	1635
150	Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu	
151	450 455 460	
153	gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa	1683
154	Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu	
155	465 470 475	
157	agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca aat	1731
158	Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn	
159	480 485 490	
161	cct ttc ctt gta gca gta cag gat tct gag gca gat tat gtt aca aca	1779
162	Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr	
163	495 500 505	
165	gat acc tta tca aag gtg act gag gca gca gtg tca aac atg cct gaa	1827
166	Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu	
167	510 515 520 525	
168	ggt ctg acg cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat	1875
169	Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn	
170	530 535 540	
172	gaa gcc aca ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc	1923
173	Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val	
174	545 550 555	
176	caa aca tca gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt	1971
177	Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu	
178	560 565 570	
180	tgc cca tca ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct	2019
181	Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro	
182	575 580 585	
184	gat att gtt atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt	2067
185	Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly	
186	590 595 600 605	
188	gct tct gta gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca	2115
189	Ala Ser Val Val Gln Pro Ser Val Pro Leu Glu Ala Pro Pro Pro	

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190	610	615	620	
192	gtt agt tat gac agt ata aag ctt gag cct gaa aac ccc cca cca tat			2163
193	Val Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr			
194	625	630	635	
196	gaa gaa gcc atg aat gta gca cta aaa gct ttg gga aca aag gaa gga			2211
197	Glu Glu Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly			
198	640	645	650	
200	ata aaa gag cct gaa agt ttt aat gca gct gtt cag gaa aca aag gct			2259
201	Ile Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala			
202	655	660	665	
204	cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc			2307
205	Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser			
206	670	675	680	685
208	act gag cca agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc			2355
209	Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe			
210	690	695	700	
212	gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct			2403
213	Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro			
214	705	710	715	
216	gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc			2451
217	Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val			
218	720	725	730	
220	cca caa aca caa gag gag gct gtg atg ctc atg aag gag agt ctc act			2499
221	Pro Gln Thr Gln Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr			
222	735	740	745	
224	gaa gtg tct gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc			2547
225	Glu Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala			
226	750	755	760	765
228	tca cct cag gag cta gga aag cca tat tta gag tct ttt cag ccc aat			2595
229	Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn			
230	770	775	780	
232	tta cat agt aca aaa gat gct gca tct aat gac att cca aca ttg acc			2643
233	Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr			
234	785	790	795	
236	aaa aag gag aaa att tct ttg caa atg gaa gag ttt aat act gca att			2691
237	Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile			
238	800	805	810	
240	tat tca aat gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa			2739
241	Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu			
242	815	820	825	
244	agt gaa aca ttt tca gat tca tct ccg att gag ata ata gat gaa ttt			2787
245	Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe			
246	830	835	840	845
248	ccc acg ttt gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag			2835
249	Pro Thr Phe Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu			
250	850	855	860	
252	tac act gat cta gaa gta tcc gac aaa agt gaa att gct aat atc caa			2883
253	Tyr Thr Asp Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln			
254	865	870	875	

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256	agc	ggg	gca	gat	tca	ttg	cct	tgc	tta	gaa	ttg	ccc	tgt	gac	ctt	tct	2931
257	Ser	Gly	Ala	Asp	Ser	Leu	Pro	Cys	Leu	Glu	Leu	Pro	Cys	Asp	Leu	Ser	
258																890	
																885	
																890	
260	ttc	aag	aat	ata	tat	cct	aaa	gat	gaa	gta	cat	gtt	tca	gat	gaa	ttc	2979
261	Phe	Lys	Asn	Ile	Tyr	Pro	Lys	Asp	Glu	Val	His	Val	Ser	Asp	Glu	Phe	
262																895	
																900	
																905	
264	tcc	gaa	aat	agg	tcc	agt	gta	tct	aag	gca	tcc	ata	tcg	cct	tca	aat	3027
265	Ser	Glu	Asn	Arg	Ser	Ser	Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	
266																910	
																915	
																920	
																925	
268	gtc	tct	gct	ttg	gaa	cct	cag	aca	gaa	atg	ggc	agc	ata	gtt	aaa	tcc	3075
269	Val	Ser	Ala	Leu	Glu	Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	Lys	Ser	
270																930	
																935	
																940	
272	aaa	tca	ctt	acg	aaa	gaa	gca	gag	aaa	aaa	ctt	cct	tct	gac	aca	gag	3123
273	Lys	Ser	Leu	Thr	Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	
274																945	
																950	
																955	
276	aaa	gag	gac	aga	tcc	ctg	tca	gct	gtt	ttg	tca	gca	gag	ctg	agt	aaa	3171
277	Lys	Glu	Asp	Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	
278																960	
																965	
																970	
280	act	tca	gtt	gtt	gac	ctc	ctc	tac	tgg	aga	gac	att	aag	aag	act	gga	3219
281	Thr	Ser	Val	Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	
282																975	
																980	
																985	
284	gtg	gtg	ttt	ggt	gcc	agc	tta	tcc	ctg	ctg	ctg	tct	ctg	aca	gtg	ttc	3267
285	Val	Val	Phe	Gly	Ala	Ser	Leu	Phe	Leu	Leu	Ser	Leu	Thr	Val	Phe		
286																990	
																995	
																1000	
																1005	
288	agc	att	gtc	agt	gta	acg	gcc	tac	att	gcc	ttg	gcc	ctg	ctc	tct	gtg	3315
289	Ser	Ile	Val	Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	
290																1010	
																1015	
																1020	
292	act	atc	agc	ttt	agg	ata	tat	aag	ggc	gtg	atc	cag	gct	atc	cag	aaa	3363
293	Thr	Ile	Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	
294																1025	
																1030	
																1035	
296	tca	gat	gaa	ggc	cac	cca	ttc	agg	gca	tat	tta	gaa	tct	gaa	gtt	gct	3411
297	Ser	Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	
298																1040	
																1045	
																1050	
300	ata	tca	gag	gaa	ttg	gtt	cag	aaa	tac	agt	aat	tct	gct	ctt	ggt	cat	3459
301	Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ala	Leu	Gly	His		
302																1055	
																1060	
																1065	
304	gtg	aac	agc	aca	ata	aaa	gaa	ctg	agg	cg	ctt	tcc	tta	gtt	gat	gat	3507
305	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	Asp	
306																1070	
																1075	
																1080	
																1085	
308	tta	gtt	gat	tcc	ctg	aag	ttt	qca	gtg	ttg	atg	tgg	gtg	ttt	act	tat	3555
309	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	Phe	Thr	Tyr	
310																1090	
																1095	
																1100	
312	gtt	ggt	gcc	ttg	tcc	aat	ggt	ctg	aca	ctt	ctg	att	tta	gct	ctg	atc	3603
313	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	Leu	Ala	Leu	Ile	
314																1105	
																1110	
																1115	
316	tca	ctc	tcc	tgt	att	tat	gaa	cg	cat	cag	gtg	cag	ata				3651
317	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile	Tyr	Glu	Arg	His	Gln	Val	Gln	Ile	
318																1120	
																1125	
																1130	
320	gat	cat	tat	cta	gga	ctt	gca	aac	aag	agt	gtt	aag	gat	gcc	atg	gcc	3699

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 2//
Seq#:6; Xaa Pos. 2,5
Seq#:29; Xaa Pos. 187,188,189,190,221,328,477
Seq#:30; Xaa Pos. 469
Seq#:35; N Pos. 110
Seq#:36; N Pos. 91
Seq#:37; N Pos. 170,275
Seq#:38; N Pos. 371,444,474,501,506,524,544,561,580,614,620
Seq#:39; N Pos. 149,198,207,246,312,317
Seq#:42; N Pos. 383,402,421,433,441
Seq#:47; N Pos. 3,6,12,15,18
Seq#:48; N Pos. 3,6,9,12,15
Seq#:49; N Pos. 3,6,12,15,20
Seq#:50; N Pos. 3,6,9,12,15,18,21
Seq#:51; N Pos. 9,12,24

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L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:176
L:977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:208
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:320
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:464
L:1169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:464
L:1358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:60
L:1375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:60
L:1395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:120
L:1397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:240
L:1416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:360
L:1417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:420
L:1418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:480
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:540
L:1420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:600
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:120
L:1436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:180
L:1437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:240
L:1438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:300
L:1483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:360
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:420
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:1562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:1579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:1596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0